

In the Specification:

Please replace the paragraph beginning at page 42, line 23, with the following:

--Various tag polypeptides and their respective antibodies are well known in the art.

Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; HIS6 (SEQ ID NO:135) and metal chelation tags, the flu HA tag polypeptide and its antibody 12CA5 [Field *et al.*, *Mol. Cell. Biol.*, 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan *et al.*, *Molecular and Cellular Biology*, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky *et al.*, *Protein Engineering*, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp *et al.*, *BioTechnology*, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin *et al.*, *Science*, 255:192-194 (1992)]; tubulin epitope peptide [Skinner *et al.*, *J. Biol. Chem.*, 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth *et al.*, *Proc. Natl. Acad. Sci. USA*, 87:6393-6397 (1990)].--

Please replace the paragraph beginning at page 82, line 3, with the following:

--AAA4 DNA sequence (SEQ ID NO:1):
Gene name: CGI-100 protein
Unigene number: Hs.275253
Probeset Accession #: AA089688
Nucleic Acid Accession #: NM_016040 cluster
Coding sequence: 142-831 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 82, line 32, with the following:

--AAA7 DNA sequence (SEQ ID NO:2):
Gene name: Endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1)
Unigene number: Hs.154210
Probeset Accession #: M31210
Nucleic Acid Accession #: NM_001400 cluster
Coding sequence: 251-1396 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 83, line 20, with the following:

95 --AAB3 DNA sequence (SEQ ID NO:3):

Gene name: Solute carrier family 20 (phosphate transporter), member 1, Human leukaemia virus receptor 1 (GLVR1)

Unigene number: Hs.78452

Probeset Accession #: L20859

Nucleic Acid Accession #: NM_005415 cluster

Coding sequence: predicted 371-2410 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 84, line 16, with the following:

20021560-423601
96 --AAB4 DNA sequence (SEQ ID NO:4):

Gene name: Matrix metalloproteinase 10 (stromelysin 2)

Unigene number: Hs.2258

Probeset Accession #: X07820

Nucleic Acid Accession #: NM_002425

Coding sequence: predicted 23-1453 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 84, line 55, with the following:

97 --AAB6 DNA sequence (SEQ ID NO:5):

Gene name: Podocalyxin-like

Unigene number: Hs.16426

Probeset Accession #: U97519

Nucleic Acid Accession #: NM_005397 cluster

Coding sequence: 251-1837 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 86, line 26, with the following:

98 --AAB8 DNA sequence (SEQ ID NO:6):

Gene name: EGF-containing fibulin-like extracellular matrix protein 1

Unigene number: Hs.76224

Probeset Accession #: U03877

Nucleic Acid Accession #: NM_004105 Transcript variant 1

Coding sequence: 150-1631 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 87, line 13, with the following:

99 --AAB9 DNA sequence (SEQ ID NO:7):

Gene name: Melanoma adhesion molecule, MUC 18 glycoprotein

Unigene number: Hs.211579

Probeset Accession #: M28882

Nucleic Acid Accession #: NM_006500 cluster

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Cat
09
Coding sequence: 27-1967 (predicted start/stop codons underlined)--

10021660-120601
T0902T-099T200T

Please replace the paragraph beginning at page 88, line 14, with the following:

--AAC1 DNA sequence (SEQ ID NO:8):

Gene name: Matrix metalloproteinase 1 (interstitial collagenase)
Unigene number: Hs.83169
Probeset Accession #: X54925
Nucleic Acid Accession #: NM_002421 cluster
Coding sequence: 69-1478 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 88, line 56, with the following:

--AAC3 DNA sequence (SEQ ID NO:9):

Gene name: Branched chain aminotransferase 1, cytosolic
Unigene number: Hs.157205
Probeset Accession #: AA423987
Nucleic Acid Accession #: NM_005504 cluster
Coding sequence: 1-1155 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 89, line 17, with the following:

--ACG4 DNA sequence (SEQ ID NO:10):

Gene name: Pentaxin-related gene, rapidly induced by IL-1 beta
Unigene number: Hs.2050
Probeset Accession #: M31166
Nucleic Acid Accession #: NM_002852 cluster
Coding sequence: 68-1213 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 89, line 57, with the following:

--ACK5 DNA sequence (SEQ ID NO:11):

Gene name: Von Willebrand factor; Coagulation factor VIII
Unigene number: Hs.110802
Probeset Accession #: M10321
Nucleic Acid Accession #: NM_000552
Coding sequence: 311-8752 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 92, line 11, with the following:

a¹⁴ --AAC7 DNA sequence (SEQ ID NO:12):

Gene name: KIAA1294 protein

Probeset Accession #: AA432248

Nucleic Acid Accession #: AB037715

Coding sequence: 370-3489 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 93, line 65, with the following:

a¹⁵ --ACG8 DNA sequence (SEQ ID NO:13):

Gene name: ubiquitin E3 ligase SMURF2

Unigene number: Hs.21806 (3'UTR only)

Probeset Accession #: AA398243

Nucleic Acid Accession #: AF301463 cluster

Coding sequence: 9-2255 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 94, line 44, with the following:

a¹⁶ --ACH1 DNA sequence (SEQ ID NO:14):

Gene name: EST

Unigene number: Hs.30089

Probeset Accession #: AA410480

CAT cluster#: 96816_1

Coding sequence: Partial sequence, possible frameshift. Predicted stop codon underlined.--

Please replace the paragraph beginning at page 95, line 2, with the following:

a¹⁷ --ACJ2 DNA sequence (SEQ ID NO:15):

Gene name: Complement component C1q receptor

Unigene number: Hs.97199

Probeset Accession #: AA487558

Nucleic Acid Accession #: NM_012072

Coding sequence: 149-2107. Predicted start/stop codons underlined--

Please replace the paragraph beginning at page 96, line 55, with the following:

--ACJ3 DNA sequence (SEQ ID NO:16):

Gene name: FLT1/vascular endothelial growth factor receptor
Unigene number: Hs.138671
Probeset Accession #: AA047437
Nucleic Acid Accession #: NM_002019
Coding sequence: 250-4266 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 98, line 56, with the following:

--ACJ9 DNA sequence (SEQ ID NO:17):

Gene name: Purine nucleoside phosphorylase
Unigene number: Hs.75514
Probeset Accession #: K02574
Nucleic acid Accession #: X00737 cluster
Coding sequence: 110-979 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 99, line 21, with the following:

--ACK4 DNA sequence (SEQ ID NOS:18 and 19):

Gene name: EST
Unigene number: Hs.265499
Probeset Accession #: R68763
CAT cluster#: Cluster 46668_2
Sequence: Both the EST corresponding to the probeset accession and exon prediction; number and the CAT cluster align with the Homo sapiens BAC clone AC009414 RP11-490M8. Using FGENESH, 2 exons predicted on this BAC clone upstream of the probeset.
Predicted exon 1: bases 5808-5837 of BAC clone AC009414--

Please replace the paragraph beginning at page 99, line 58, with the following:

--Predicted ACK4 gene seq (predicted start/stop codons underlined) (SEQ ID NO:19):--

Please replace the paragraph beginning at page 100, line 20, with the following:

a22
--AAA8 DNA sequence (SEQ ID NO:20):

Gene name: ETL protein, with extended open reading frame

Unigene number: Hs.57958

Probeset Accession #: D58024

Nucleotide Accession #: AF192403

Coding sequence: 151-2136. Underlined sequences correspond to extended sequence not included in AF192403.--

Please replace the paragraph beginning at page 101, line 11, with the following:

a23
--AAC6 DNA sequence (SEQ ID NO:21):

Gene name: Homo sapiens cDNA FLJ13465 fis, clone PLACE1003493, weakly similar to endothelial cell multimerin precursor

Unigene number: Hs.134797

Probeset Accession #: AA025351

Nucleotide Accession #: AK023527

Coding sequence: predicted 75-2921

Extended sequence: 729-3465 (underlined sequence)--

Please replace the paragraph beginning at page 102, line 18, with the following:

a24
--ACH7 DNA sequence (SEQ ID NOS:22-24):

Gene name: ESTs

Unigene number: Hs.3807

Probeset Accession #: AA292694

BAC Accession #: AL161751

FGENESH predicted exons: FGENESH predicts 2 exons on the minus strand of AL161751 upstream of the ACH7 probeset.--

Please replace the paragraph beginning at page 102, line 26, with the following:

a25
--FGENESH predicted exon 1 (SEQ ID NO:22):--

Please replace the paragraph beginning at page 102, line 32, with the following:

a26
--FGENESH predicted exon 2 (SEQ ID NO:23):--

Please replace the paragraph beginning at page 102, line 63, with the following:

Q27 --ACH7 predicted coding seq (predicted start/stop codons underlined) (SEQ ID NO:24) :--

Please replace the paragraph beginning at page 103, line 31, with the following:

Q28 --AAD3 DNA sequence (SEQ ID NO:25) :
Gene name: ESTs
Unigene number: Hs.17404
Probeset Accession #: N39584
Nucleic Acid Accession #: N39584
Coding sequence: no identified ORF; possible frameshifts--

Please replace the paragraph beginning at page 103, line 64, with the following:

Q29 --AAD4 DNA sequence (SEQ ID NO:26) :
Gene name: ERG
Unigene number: Hs.279477 / Hs.45514
Probeset Accession #: R32894
Nucleic Acid Accession #: M17254
Coding sequence: 257-1645 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 104, line 58, with the following:

Q30 --AAD5 DNA sequence (SEQ ID NO:27) :
Gene name: activin A receptor type II-like 1 (ALK-1)
Unigene number: Hs.8881 / Hs.172670
Probeset Accession #: T57112
Nucleic Acid Accession #: NM_000020
Coding sequence: 283-1794 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 106, line 3, with the following:

Q31 --AAD8 DNA sequence (SEQ ID NO:28) :
Gene name: ESTs
Unigene number: Hs.144953
Probeset Accession #: AA404418
Nucleic Acid Accession #: n/a
Coding sequence: no ORF identified; possible frameshifts--

Please replace the paragraph beginning at page 106, line 39, with the following:

--ACA2 DNA sequence (SEQ ID NO:29):

Gene name: EST

Unigene number: Hs.16450

Probeset Accession #: AA478778

Nucleic Acid Accession #: AA478778

Coding sequence: no ORF identified; possible frameshifts--

Please replace the paragraph beginning at page 107, line 1, with the following:

--ACA4 DNA sequence (SEQ ID NO:30):

Gene name: alpha satellite junction DNA sequence

Unigene number: Hs.247946

Probeset Accession #: M21305

Nucleic Acid Accession #: M21305

Coding sequence: 1-165 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 107, line 13, with the following:

--ACG6 DNA sequence (SEQ ID NO:31):

Gene name: intercellular adhesion molecule 2 (ICAM2)

Unigene number: Hs.83733

Probeset Accession #: M32334

Nucleic Acid Accession #: NM_000873

Coding sequence: 63-890 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 107, line 40, with the following:

--ACG7 DNA sequence (SEQ ID NO:32):

Gene name: Cadherin 5, VE-cadherin (CDH5)

Unigene number: Hs.76206

Probeset Accession #: X79981

Nucleic Acid Accession #: NM_001795

Coding sequence: 25-2379 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 108, line 48, with the following:

--ACG9 DNA sequence (SEQ ID NO:33):

Gene name: lysyl oxidase-like 2 (LOXL2)

Unigene number: Hs.83354

Probeset Accession #: U89942

Nucleic Acid Accession #: NM_002318 cluster

Coding sequence: 248-2572 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 109, line 47, with the following:

--ACH2 DNA sequence (SEQ ID NO:34):

Gene name: TIE tyrosine-protein kinase

Unigene number: Hs.78824

Probeset Accession #: X60957

Nucleic Acid Accession #: NM_005424 cluster

Coding sequence: 37-3452 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 110, line 53, with the following:

--ACH3 DNA sequence (SEQ ID NO:35):

Gene name: placental growth factor (PGF; PlGF1; VEGF-related protein)

Unigene number: Hs.2894

Probeset Accession #: X54936

Nucleic Acid Accession #: NM_002632 cluster

Coding sequence: 322-768 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 111, line 22, with the following:

--ACH4 DNA sequence (SEQ ID NO:36):

Gene name: nidogen 2 (NID2)

Unigene number: Hs.82733

Probeset Accession #: D86425

Nucleic Acid Accession #: NM_007361 cluster

Coding sequence: 1-4131 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 112, line 44, with the following:

--ACH5 DNA sequence (SEQ ID NO:37):

Gene name: SNL (singled-like; sea urchin fascin homolog-like)

Unigene number: Hs.118400

Probeset Accession #: U03057

Nucleic Acid Accession #: NM_003088

Coding sequence: 112-1593 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 113, line 32, with the following:

--ACH6 DNA sequence (SEQ ID NO:38):

Gene name: endothelial protein C receptor (EPCR; PROCR)

Unigene number: Hs.82353

Probeset Accession #: L35545

Nucleic Acid Accession #: NM_006404

Coding sequence: 25-741 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 113, line 63, with the following:

--ACH8 DNA sequence (SEQ ID NO:39):

Gene name: melanoma adhesion molecule (MCAM; MUC18)

Unigene number: Hs.211579

Probeset Accession #: D51069

Nucleic Acid Accession #: NM_006500

Coding sequence: 27-1967 (predicted start and stop codons underlined)--

Please replace the paragraph beginning at page 114, line 64, with the following:

--ACH9 DNA sequence (SEQ ID NO:40):

Gene name: endothelin-1 (EDN1)

Unigene number: Hs.2271

Probeset Accession #: J05008

Nucleic Acid Accession #: NM_001955

Coding sequence: 337-975 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 115, line 26, with the following:

--ACJ1 DNA sequence (SEQ ID NO:41):

Gene name: BMX non-receptor tyrosine kinase

Unigene number: Hs.27372

Probeset Accession #: X83107

Nucleic Acid Accession #: NM_001721

Coding sequence: 34-2061 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 116, line 8, with the following:

--ACJ4 DNA sequence (SEQ ID NO:42):

Gene name: prostaglandin G/H synthase 2 (COX-2; PGHS-2)

Unigene number: Hs.196384

Probeset Accession #: D28235

Nucleic Acid Accession #: NM_000963

Coding sequence: 135-1949 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 117, line 24, with the following:

--ACJ6 DNA sequence (SEQ ID NO:43):

Gene name: SEC14-like-1

Unigene number: Hs.75232

Probeset Accession #: D67029

Nucleic Acid Accession #: NM_003003

Coding sequence: 304-2451 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 118, line 56, with the following:

--ACJ8 DNA sequence (SEQ ID NO:44):

Gene name: intercellular adhesion molecule 1 (ICAM1; CD54)

Unigene number: Hs.168383

Probeset Accession #: M24283

Nucleic Acid Accession #: NM_000201

Coding sequence: 58-1656 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 119, line 47, with the following:

Q48
--ACK3 DNA sequence (SEQ ID NO:45):
Gene name: angiopoietin 1 receptor (TIE-2; TEK)
Unigene number: Hs.89640
Probeset Accession #: L06139
Nucleic Acid Accession #: NM_000459
Coding sequence: 149-3523 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 120, line 57, with the following:

Q49
10021660-12001
--PZA6 DNA sequence (SEQ ID NO:46):
Gene name: prostate differentiation factor (PLAB; MIC-1)
Unigene number: Hs.116577
Probeset Accession #: AB000584
Nucleic Acid Accession #: NM_004864
Coding sequence: 26-952 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 121, line 19, with the following:

Q50
10021660-12001
--AAC8 DNA sequence (SEQ ID NO:47):
Gene name: none
Unigene number: Hs.6682
Probeset Accession #: AA227926
Nucleic Acid Accession #: none
Coding sequence: no ORF identified, possible frameshifts--

Please replace the paragraph beginning at page 122, line 12, with the following:

Q51
--AAD2 DNA sequence (SEQ ID NO:48):
Gene name: Thrombospondin-1
Unigene number: Hs.87409
Probeset Accession #: AA232645
Nucleic Acid Accession #: NM_003246
Coding sequence: 112-3624 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 123, line 49, with the following:

Q52 --AAD9 DNA sequence (SEQ ID NO:49):

Gene name: LIM homeobox protein cofactor (CLIM-1)

Unigene number: Hs.4980

Probeset Accession #: F13782

Nucleic Acid Accession #: AF047337

Coding sequence: 110-1231(predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 124, line 29, with the following:

Q53 --AAE1 DNA sequence (SEQ ID NO:50):

Gene name: guanine nucleotide binding protein 11

Unigene number: Hs.83381

Probeset Accession #: U31384

Nucleic Acid Accession #: NM_004126.1

Coding sequence: 108-329 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 124, line 49, with the following:

Q54 --AAE2 DNA sequence (SEQ ID NO:51):

Gene name: Transcription factor 4 (immunoglobulin transcription factor 2) (ITF-2) (SL3-3 Enhancer factor 2) (SEF-2)

Unigene number: Hs.289068

Probeset Accession #: M74719

Nucleic Acid Accession #: NM_003199.1

Coding sequence: 200-2203 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 125, line 33, with the following:

Q55 --AAE4 DNA sequence (SEQ ID NO:52):

Gene name: phosphatidylcholine 2-acylhydrolase

Unigene number: Hs.211587

Probeset Accession #: M68874

Nucleic Acid Accession #: M68874

Coding sequence: 139-2388 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 126, line 22, with the following:

Q56 --ACA1 DNA sequence (SEQ ID NO:53):

Gene name: tissue factor pathway inhibitor 2 TFPI2, placental protein 5 (PP5)

Unigene number: Hs.78045

Probeset Accession #: D29992

Nucleic Acid Accession #: D29992.1

Coding sequence: 57-764 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 126, line 51, with the following:

Q57 --ACB8 DNA sequence (SEQ ID NO:54):

Gene name: myosin X

Unigene number: Hs.61638

Probeset Accession #: N77151

Nucleic Acid Accession #: NM_012334

Coding sequence: 223-6399 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 128, line 54, with the following:

Q58 --ACC3 DNA sequence (SEQ ID NO:55):

Gene name: calcitonin receptor-like (CALCRL)

Unigene number: Hs.152175

Probeset Accession #: L76380

Nucleic Acid Accession #: NM_005795

Coding sequence: 555-1940 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 129, line 46, with the following:

Q59 --ACC4 DNA sequence (SEQ ID NO:56):

Gene name: Homo sapiens mRNA; cDNA DKFZp586E1624

Unigene number: Hs.94030

Probeset Accession #: AA452000

Nucleic Acid Accession #: AL110152.1

Coding sequence: no ORF identified, possible frameshifts--

Please replace the paragraph beginning at page 130, line 10, with the following:

Q160
--ACC5 DNA sequence (SEQ ID NO:57):
Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Nucleic Acid Accession #: NM_000450
Coding sequence: 117-1949 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 131, line 15, with the following:

Q161
--ACC8 DNA sequence (SEQ ID NO:58):
Gene name: Chemokine (C-X-C motif), receptor 4 (fusin)
Unigene number: Hs.89414
Probeset Accession #: L06797
Nucleic Acid Accession #: NM_003467
Coding sequence: 89-1147 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 131, line 52, with the following:

Q162
--ACF2 DNA sequence (SEQ ID NO:59):
Gene name: Endothelial cell-specific molecule 1
Unigene number: Hs.41716
Probeset Accession #: X89426
Nucleic Acid Accession #: NM_007036
Coding sequence: 56-610 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 132, line 27, with the following:

Q163
--ACF4 DNA sequence (SEQ ID NO:60):
Gene name: P53-responsive gene 2 similar to D.melanogaster peroxidase(U11052)
Unigene number: Hs.118893
Probeset Accession #: D86983
Nucleic Acid Accession #: D86983
Coding sequence: 1-4491 (predicted stop codon underlined, sequence is open at 5' end)--

Please replace the paragraph beginning at page 133, line 61, with the following:

Q64
--ACF5 DNA sequence (SEQ ID NO:61):

Gene name: Mitogen-activated protein kinase kinase kinase 4
Unigene number: Hs.3628
Probeset Accession #: N54067
Nucleic Acid Accession #: NM_004834
Coding sequence: 80-3577 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 134, line 67, with the following:

Q65
--ACF8 DNA sequence (SEQ ID NO:62):

Gene name: Phospholipase A2, group IVC (cytosolic, calcium-independent)
Unigene number: Hs.18858
Probeset Accession #: AA054087
Nucleic Acid Accession #: NM_003706
Coding sequence: 310-1935 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 135, line 50, with the following:

Q66
--ACG1 DNA sequence (SEQ ID NO:63):

Gene name: Carbohydrate (chondroitin 6/keratan) sulfotransferase 1
Unigene number: Hs.104576
Probeset Accession #: AA868063
Nucleic Acid Accession #: NM_003654
Coding sequence: 367-1602 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 136, line 32, with the following:

Q67
--ACG5 DNA sequence (SEQ ID NO:64):

Gene name: Multimerin
Unigene number: Hs.268107
Probeset Accession #: U27109
Nucleic Acid Accession #: U27109.1
Coding sequence: 72-3758 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 137, line 43, with the following:

--ACC6 DNA sequence (SEQ ID NO:65):

Gene name: Homo sapiens cDNA FLJ11502 fis, clone HEMBA1002102, weakly similar to ANKRYIN

Unigene number: Hs.213194

Probeset Accession #: AA187101

Nucleic Acid Accession #: AK021564

Coding sequence: 1-450 (predicted stop codon underlined, 5'end sequence is open)--

Please replace the paragraph beginning at page 138, line 13, with the following:

--ACC7 DNA sequence (SEQ ID NO:66):

Gene name: Human RAL A gene

Unigene number: Hs.6906

Probeset Accession #: AA083572

Nucleic Acid Accession #: contig of X15014.1 and AK026850

Coding sequence: 1-621 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 138, line 65, with the following:

--ACC9 DNA sequence (SEQ ID NO:67):

Gene name: KIAA0955 protein

Unigene number: Hs.10031

Probeset Accession #: AA027168

Nucleic Acid Accession #: AB023172

Coding sequence: 314-1609 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 140, line 23, with the following:

--ACF6 DNA sequence (SEQ ID NO:68):

Gene name: Homo sapiens cDNA FLJ10669 fis, clone NT2RP2006275, weakly similar to Microtubule-associated protein 1B [CONTAINS: LIGHT CHAIN LC1]

Unigene number: Hs.66048

Probeset Accession #: AA609717

Nucleic Acid Accession #: AK001531

Coding sequence: 176-2194 (predicted start/stop codons underlined)--

Please replace the paragraph beginning at page 141, line 4, with the following:

--AAA4 Protein sequence (SEQ ID NO:69):

Gene name: CGI-100 protein

Unigene number: Hs.275253

Probeset Accession #: AA089688

Protein Accession #: NP_057124

Signal sequence: predicted 1-23 (first underlined sequence)

Transmembrane Domain: predicted 201-217 (second underlined sequence)

emp24/gp25L/p24 domain: predicted 13-227

Summary: gp25L/emp24/p24 protein family members of the cis-Golgi network bind both COP I and II coatomer. Members of this family are implicated in bringing cargo forward from the ER and binding to coat proteins by their cytoplasmic domains.--

Please replace the paragraph beginning at page 141, line 22, with the following:

--AAA7 Protein sequence (SEQ ID NO:70):

Gene name: Endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 (EDG1)

Unigene number: Hs.154210

Probeset Accession #: M31210

Protein Accession#: NP_001391

7 Transmembrane Domains: predicted 50-71, 92-110, 122-140, 160-177, 201-222, 251-269, 281-301 (underlined sequences)

Summary: Endothelial differentiation, sphingolipid G-protein-coupled receptor, 1 may regulate the differentiation of endothelial cells. It binds the sphingolipid metabolite, sphingosine-1-phosphate, which may function as a second messenger in cell proliferation and survival.--

Please replace the paragraph beginning at page 141, line 44, with the following:

--AAB3 Protein sequence (SEQ ID NO:71):

Gene name: Solute carrier family 20 (phosphate transporter), member 1, Human leukaemia virus receptor 1 (GLVR1)

Unigene number: Hs.78452

Probeset Accession #: L20859

Protein Accession #: NP_005406

Transmembrane domains: predicted 24-40, 62-78, 164-180, 198-214, 232-248, 513-529, 562-578, 604-620, 655-671

Cellular Localization: Likely a Type IIIa membrane protein (Ncyt Cexo)--

Please replace the paragraph beginning at page 141, line 68, with the following:

Q⁷⁵
--AAB4 Protein sequence (SEQ ID NO:72):
Gene name: Matrix metalloproteinase 10 (stromelysin 2)
Unigene number: Hs.2258
Probeset Accession #: X07820
Protein Accession #: NP_002416
Signal sequence: predicted 1-17 (underlined sequence)
Cellular Localization: predicted secreted--

Please replace the paragraph beginning at page 142, line 18, with the following:

Q⁷⁶
--AAB6 Protein sequence (SEQ ID NO:73):
Gene name: Podocalyxin-like
Unigene number: Hs.16426
Probeset Accession #: U97519
Protein Accession #: NP_005388
Transmembrane domain: predicted 432-448 (underlined sequence)
Cellular Localization: predicted Type Ia membrane protein (Nexo)--

Please replace the paragraph beginning at page 142, line 37, with the following:

Q⁷⁷
--AAB8 Protein sequence (SEQ ID NO:74):
Gene name: EGF-containing fibulin-like extracellular matrix protein 1
Unigene number: Hs.76224
Probeset Accession #: U03877
Protein Accession #: NP_004096 Variant 1
Signal sequence: predicted 1-17 (underlined sequence)
Summary: This gene spans approximately 18 kb of genomic DNA and consists of 12 exons. Two transcripts with distinct 5' UTR have been described; the resulting proteins have distinct N-terminal amino acid sequences. Translation initiation from internal methionine residues was observed with in vitro translation. A signal peptide sequence is predicted for translation initiation sites 1, 2, and 4. The protein isoforms contain 5 or 6 calcium-binding EGF2 domains and 5 or 6 EGF2 domains. Mutations in this gene cause the retinal disease Malattia Leventinese. Transcript Variant: This variant (1) has a distinct 5' UTR and N-terminal protein sequence as compared to variant 2.--

Please replace the paragraph beginning at page 142, line 64, with the following:

Q78
--AAB9 Protein sequence (SEQ ID NO:75):
Gene name: Melanoma adhesion molecule, MUC 18 glycoprotein
Unigene number: Hs.211579
Probeset Accession #: M28882
Protein Accession #: NP_006491
Signal sequence: predicted 1-17 (first underlined sequence)
Transmembrane domain: predicted 559-575 (second underlined sequence)
Cellular localization: predicted Type Ia membrane protein (Nexo)--

Please replace the paragraph beginning at page 143, line 18, with the following:

Q79
--AAC1 Protein sequence (SEQ ID NO:76):
Gene name: Matrix metalloproteinase 1 (interstitial collagenase)
Unigene number: Hs.83169
Probeset Accession #: X54925
Protein Accession #: NP_002412
Signal sequence: predicted 1-19 (underlined sequence)
Cellular localization: predicted secreted protein--

Please replace the paragraph beginning at page 143, line 36, with the following:

Q80
--AAC3 Protein sequence (SEQ ID NO:77):
Gene name: Branched chain aminotransferase 1, cytosolic
Unigene number: Hs.157205
Probeset Accession #: AA423987
Protein Accession #: NP_005495
Cellular Localization: cytoplasmic
Summary: The lack of the cytosolic enzyme branched-chain amino acid transaminase (BCT) causes cell growth inhibition. There may be at least 2 different clinical disorders due to a defect of branched-chain amino acid transamination: hypervalinemia and hyperleucine-isoleucinemia. Since there are 2 distinct BCATs, mitochondrial and cytosolic, it is possible that one is mutant in each of these 2 conditions.--

Please replace the paragraph beginning at page 143, line 58, with the following:

Q81
--ACG4 Protein sequence (SEQ ID NO:78):

Gene name: Pentaxin-related gene, rapidly induced by IL-1 beta

Unigene number: Hs.2050

Probeset Accession #: M31166

Protein Accession #: NP_002843

Signal sequence: predicted 1-17 (underlined sequence)

Cellular localization: predicted secreted

Summary: TNF-inducible member of hyaluronate binding protein family, related to CD44--

Please replace the paragraph beginning at page 144, line 9, with the following:

Q82
--ACK5 Protein sequence (SEQ ID NO:79):

Gene name: Von Willebrand factor; Coagulation factor VIII

Unigene number: Hs.110802

Probeset Accession #: M10321

Protein Accession #: NP_000543

Signal peptide: predicted 1-22 (underlined sequence)

Cellular localization: predicted secreted--

Please replace the paragraph beginning at page 144, line 66, with the following:

Q83
--AAC7 protein sequence (SEQ ID NO:80):

Gene name: KIAA1294 protein

Probeset Accession #: AA432248

Protein Accession #: BAA92532

Cellular localization: predicted nuclear protein

PFAM prediction: 22-153 Band 41 domain (underlined seq). A number of cytoskeletal-associated proteins that associate with various proteins at the interface between the plasma membrane and the cytoskeleton contain a conserved N-terminal domain of about 150 amino-acid residues.--

Please replace the paragraph beginning at page 145, line 28, with the following:

Q84
--ACG8 Protein sequence (SEQ ID NO:81):

Gene name: ubiquitin E3 ligase SMURF2

Unigene number: Hs.21806 (3'UTR only)

Probeset Accession #: AA398243

Protein Accession #: AF301463_1

Cellular Localization: predicted cytoplasmic

Summary: Smurf2 Is a Ubiquitin E3 Ligase Mediating Proteasome-dependent Degradation of Smad2 in Transforming Growth Factor-beta Signaling--

Please replace the paragraph beginning at page 145, line 52, with the following:

985
--ACH1 Protein sequence (SEQ ID NO:82):
Gene name: EST
Unigene number: Hs.30089
Probeset Accession #: AA410480
CAT cluster#: cluster 96816_1
Summary: predicted open reading frame--

Please replace the paragraph beginning at page 145, line 65, with the following:

986
1001660.120601
--ACJ2 Protein sequence (SEQ ID NO:83):
Gene name: Complement component C1q receptor
Unigene number: Hs.97199
Probeset Accession #: AA487558
Protein Accession #: NP_036204
Signal sequence: 1-17 (first underlined sequence)
Transmembrane domain: 589-605 (second underlined sequence)
Cellular localization: This gene encodes a predicted type I membrane protein.
Summary: This protein acts as a receptor for complement protein C1q, mannose-binding lectin, and pulmonary surfactant protein A. This protein is a functional receptor involved in ligand-mediated enhancement of phagocytosis.--

Please replace the paragraph beginning at page 146, line 22, with the following:

987
--ACJ3 Protein sequence (SEQ ID NO:84):
Gene name: FLT1/vascular endothelial growth factor receptor
Unigene number: Hs.138671
Probeset Accession #: AA047437
Transmembrane domain: predicted 764-780 (underlined sequence)
Cellular Localization: predicted cell surface tyrosine kinase--

Please replace the paragraph beginning at page 146, line 54, with the following:

988
--ACJ9 Protein sequence (SEQ ID NO:85):
Gene name: Purine nucleoside phosphorylase
Unigene number: Hs.75514
Probeset Accession #: K02574
Protein Accession #: CAA25320
Cellular Localization: predicted cytoplasmic
Summary: likely to catalyze the reversible phosphorolytic cleavage of purine ribonucleosides and 2'-deoxyribonucleosides--

Please replace the paragraph beginning at page 147, line 2, with the following:

--ACK4 Protein sequence (SEQ ID NO:86):

Gene name: EST

Probeset Accession #: R68763

Predicted amino acid seq: FGENESH exon prediction on BAC clone AC009414

Predicted nuclear target motifs: from 25 (4) RRRP (SEQ ID NO:87) (underlined);
176 (5) RRRR (SEQ ID NO:88) (underlined); 177 (5) RRRR (SEQ ID NO:88)
(underlined; 239 (5) KRKK (SEQ ID NO:89) (underlined); 399 (4) PPRARRT (SEQ ID
NO:90) (underlined); 400 (5) PRARRTE (SEQ ID NO:91) (underlined)

Cellular localization: predicted nuclear--

Please replace the paragraph beginning at page 147, line 22, with the following:

--AAA8 Protein sequence (SEQ ID NO:92):

Gene name: ETL protein, with extended open reading frame

Unigene number: Hs.57958

Probeset Accession #: D58024

Protein Accession #: AAG33021

Transmembrane domains: predicted 454-470, 486-502, 511-527, 528-544, 556-572,
600-616, 642-661, 672-689 (underlined sequences)

Extended sequence: Residues 1-564 were added to the sequence in AAG33021

Cellular Localization: predicted cell surface serpentine receptor--

Please replace the paragraph beginning at page 147, line 46, with the following:

--AAC6 Protein sequence (SEQ ID NO:93):

Gene name: EST

Unigene number: Hs.134797

Probeset Accession #: AA025351

Protein accession #: BAB14599

Signal sequence: predicted 1-24 (first underlined sequence)

extended sequence: second underlined sequence--

Please replace the paragraph beginning at page 148, line 4, with the following:

--ACH7 Protein sequence (SEQ ID NO:94):

Gene name: EST

Unigene number: Hs.3807

Probeset Accession #: AA292694

BAC Accession #: AL161751

FGENESH predicted aa seq: 1-647; based on BAC clone AL161751--

Please replace the paragraph beginning at page 148, line 24, with the following:

--AAD4 Protein sequence (SEQ ID NO:95):

Gene name: ERG

Unigene number: Hs.45514

Probeset Accession #: R32894

Protein Accession #: AAA52398

Signal sequence: none

Transmembrane domains: none

PFAM domains: predicted Ets-domain 294-373; SAM_PNT: 122-206

Summary: ERG2 is a sequence-specific DNA-binding protein.--

Please replace the paragraph beginning at page 148, line 44, with the following:

--AAD5 Protein sequence (SEQ ID NO:96):

Gene name: activin A receptor type II-like 1 (ALK-1)

Unigene number: Hs.172670

Probeset Accession #: T57112

Protein Accession #: NP_000011

Signal sequence: predicted 1-21

Transmembrane domain: predicted 119-135

PFAM domains: predicted pkinase 204-489

Summary: Type Ia membrane protein; receptor tyrosine kinase--

Please replace the paragraph beginning at page 149, line 21, with the following:

--ACA4 Protein sequence (SEQ ID NO:97):

Gene name: alpha satellite junction DNA sequence

Unigene number: Hs.247946

Probeset Accession #: M21305

Protein Accession #: AAA88020

Signal sequence: none

Transmembrane domains: none

PFAM domains: none--

Please replace the paragraph beginning at page 149, line 33, with the following:

--ACG6 Protein sequence (SEQ ID NO:98):

Gene name: intercellular adhesion molecule 2 (ICAM2)

Unigene number: Hs.83733

Probeset Accession #: M32334

Protein Accession #: NP_000864

Signal sequence: predicted 1-21

Transmembrane domain: predicted 224-248

PFAM domains: predicted 41-98, 127-197; immunoglobulin-like C2-type domains

Summary: a predicted Type Ia membrane protein; it plays a role in cell adhesion and is the ligand for the LFA-1 protein. ICAM2 is also called CD102.--

Please replace the paragraph beginning at page 149, line 51, with the following:

--ACG7 Protein sequence (SEQ ID NO:99):

Gene name: Cadherin 5, VE-cadherin (CDH5)

Unigene number: Hs.76206

Probeset Accession #: X79981

Protein Accession #: NP_001786

Signal sequence: predicted 1-27

Transmembrane domain: predicted 604-620

PFAM domains: Cadherin domains predicted 53-141, 156-249, 263-364, 377-470, and 487-576

Summary: Likely a Type I membrane protein. Cadherins are calcium-dependent adhesive proteins that mediate cell-to-cell interaction. VE-cadherin is associated with intercellular junctions.--

Please replace the paragraph beginning at page 150, line 12, with the following:

--ACG9 Protein sequence (SEQ ID NO:100):

Gene name: lysyl oxidase-like 2 (LOXL2)

Unigene number: Hs.83354

Probeset Accession #: U89942

Protein Accession #: NP_002309

Signal sequence: predicted 1-25

Transmembrane domains: none predicted

PFAM domains: scavenger receptor cysteine-rich domains predicted 68-159, 203-238, 336-425, 439-528; Lysyl oxidase predicted 548-749.

Summary: Likely a secreted protein. Lysyl oxidase is a copper-dependent amine oxidase that belongs to a heterogeneous family of enzymes that oxidize primary amine substrates to reactive aldehydes, acting on the extracellular matrix substrates, e.g., collagen and elastin.--

Please replace the paragraph beginning at page 150, line 41, with the following:

Q99
--ACH2 Protein sequence (SEQ ID NO:101):
Gene name: TIE tyrosine-protein kinase
Unigene number: Hs.78824
Probeset Accession #: X60957
Protein Accession #: NP_005415
Signal sequence: predicted 1-21
Transmembrane domain: predicted 770-786
PFAM domains: laminin-EGF predicted 234-267; FN3 predicted 460-520, 548-632, and 644-729; tyrosine_kinase predicted 839-1107
Summary: Likely a Type Ia membrane protein; TIE is a tyrosine-kinase receptor with an unknown ligand; its expression is likely necessary for normal blood vessel development.--

Please replace the paragraph beginning at page 151, line 7, with the following:

Q100
--ACH3 Protein sequence (SEQ ID NO:102):
Gene name: placental growth factor (PGF; PlGF1; VEGF-related protein)
Unigene number: Hs.2894
Probeset Accession #: X54936
Protein Accession #: NP_002623
Signal sequence: predicted 1-21
Transmembrane domain: none predicted
PFAM domains: PDGF predicted 52-130
Summary: Likely a secreted protein; likely regulates angiogenesis by interacting with FLT1 and FLK1.--

Please replace the paragraph beginning at page 151, line 23, with the following:

Q101
--ACH4 Protein sequence (SEQ ID NO:103):
Gene name: nidogen 2 (NID2)
Unigene number: Hs.82733
Probeset Accession #: D86425
Protein Accession #: NP_031387
Signal sequence: predicted 1-30
Transmembrane domain: none predicted
PFAM domains: EGF-like_domains predicted 489-524, 764-800, 806-843, 853-891, and 897-930; thyroglobulin_repeats predicted 941-1006, and 1020-1085; LDL_receptor_repeats predicted 1155-1197, 1199-1240, and 1242-1285.
Summary: A secreted protein; NID2 likely interacts with collagens I and IV and laminin-1 to promote cell adhesion to the basement membrane.--

Please replace the paragraph beginning at page 151, line 61, with the following:

--ACH5 Protein sequence (SEQ ID NO:104):

Gene name: SNL (singled-like; sea urchin fascin homolog-like)

Unigene number: Hs.118400

Probeset Accession #: U03057

Protein Accession #: NP_003079

Signal sequence: none identified

Transmembrane domain: none identified

PFAM domains: none identified

Summary: a cytoplasmic, actin-bundling protein that is likely to be involved in the assembly of actin filament bundles present in microspikes, membrane ruffles, and stress fibers--

Please replace the paragraph beginning at page 152, line 16, with the following:

--ACH6 Protein sequence (SEQ ID NO:105):

Gene name: endothelial protein C receptor (EPCR; PROCR)

Unigene number: Hs.82353

Probeset Accession #: L35545

Protein Accession #: NP_006395

Signal sequence: predicted 1-17

Transmembrane domain: predicted 211-227

PFAM domains: none identified

Summary: a Type Ia membrane protein, EPCR likely binds to [thrombin]-activated Protein C, a vitamin K-dependent serine protease zymogen necessary for blood coagulation.--

Please replace the paragraph beginning at page 152, line 34, with the following:

--ACH8 Protein sequence (SEQ ID NO:106):

Gene name: melanoma adhesion molecule (MCAM; MUC18)

Unigene number: Hs.211579

Probeset Accession #: D51069

Protein Accession #: NP_006491

Signal sequence: predicted 1-17

Transmembrane domain: predicted 559-575

PFAM domains: immunoglobulin_domains predicted 264-324, and 356-410.

Summary: a Type Ia membrane protein, associated with tumor progression and the development of metastasis in human malignant melanoma, and may play a role in neural crest cells during embryonic development.--

Please replace the paragraph beginning at page 152, line 59, with the following:

a¹⁰⁵
--ACH9 Protein sequence (SEQ ID NO:107):
Gene name: endothelin-1 (EDN1)
Unigene number: Hs.2271
Probeset Accession #: J05008
Protein Accession #: NP_001946
Signal sequence: predicted 1-17
Transmembrane domain: none predicted
PFAM domains: Endothelin domains predicted 59-73, and 108-129.
Summary: a secreted zymogen; the active protein is likely a 26-amino acid peptide with potent mammalian vasoconstrictor activity; it is necessary for normal vessel development.--

100216661.120601
a¹⁰⁶
Please replace the paragraph beginning at page 153, line 11, with the following:

--ACJ1 Protein sequence (SEQ ID NO:108):
Gene name: BMX non-receptor tyrosine kinase
Unigene number: Hs.27372
Probeset Accession #: X83107
Protein Accession #: NP_001712
Signal sequence: none identified
Transmembrane domain: none identified
PFAM domains: plektrin_homology_domain predicted 6-111; SH2_domain predicted 294-383; protein_kinase_domain predicted 417-663
Summary: a cytoplasmic protein, it likely plays a role in the growth and differentiation of hematopoietic cells; it is known to also be expressed in endothelial cells.--

Please replace the paragraph beginning at page 153, line 38, with the following:

a¹⁰⁷
--ACJ4 Protein sequence (SEQ ID NO:109):
Gene name: prostaglandin G/H synthase 2 (COX-2; PGHS-2)
Unigene number: Hs.196384
Probeset Accession #: D28235
Protein Accession #: NP_000954
Signal sequence: predicted 1-17
Transmembrane domain: none identified
PFAM domains: EGF-like_domain predicted 18-55.
Summary: a microsomal enzyme; COX-2 is the therapeutic target of the nonsteroidal anti-inflammatory drugs (NSAIDs), such as aspirin.--

Please replace the paragraph beginning at page 153, line 62, with the following:

--ACJ6 Protein sequence (SEQ ID NO:110):

Gene name: SEC14-like-1
Unigene number: Hs.75232
Probeset Accession #: D67029
Protein Accession #: NP_002994
Signal sequence: none identified
Transmembrane domain: none identified
PFAM domains: none identified
Summary: a cytoplasmic protein--

Please replace the paragraph beginning at page 154, line 18, with the following:

--ACJ8 Protein sequence (SEQ ID NO:111):

Gene name: intercellular adhesion molecule 1 (ICAM1; CD54)
Unigene number: Hs.168383
Probeset Accession #: M24283
Protein Accession #: NP_000192
Signal sequence: predicted 1-27
Transmembrane domain: predicted 481-497
PFAM domains: immunoglobulin_domains predicted 128-188, and 325-373.
Summary: a Type Ia membrane protein; ICAM1 is typically expressed on endothelial cells and cells of the immune system; ICAM1 binds to integrins of type CD11a/CD18, or CD11b/CD18; ICAM1 is also exploited by Rhinovirus as a receptor.--

Please replace the paragraph beginning at page 154, line 41, with the following:

--ACK3 Protein sequence (SEQ ID NO:112):

Gene name: angiopoietin 1 receptor (TIE-2; TEK)
Unigene number: Hs.89640
Probeset Accession #: L06139
Protein Accession #: NP_000450
Signal sequence: predicted 1-18
Transmembrane domain: predicted 746-770
PFAM domains: immunoglobulin_domains predicted 44-102, 370-424; EGF_like_domains predicted 210-252, 254-299, and 301-341; FN3_domains predicted 444-536, 541-634, and 638-732; protein_kinase_domain predicted 824-1096.
Summary: a Type Ia membrane protein; it is expressed almost exclusively in endothelial cells in mice, rats, and humans; the ligand for this receptor is angiopoietin-1; defects in TEK are associated with inherited venous malformations; the TEK signaling pathway appears to be critical for endothelial cell-smooth muscle cell communication in venous morphogenesis.--

Please replace the paragraph beginning at page 155, line 10, with the following:

all
--PZA6 Protein sequence (SEQ ID NO:113):
Gene name: prostate differentiation factor (PLAB; MIC-1)
Unigene number: Hs.116577
Probeset Accession #: AB000584
Protein Accession #: NP_004855
Signal sequence: predicted 1-29
Transmembrane domain: none identified
PFAM domains: TGF-beta _domain predicted 211-308.
Summary: a secreted protein; its exact function is unclear; it inhibits proliferation of primitive hematopoietic progenitors; it inhibits activation of macrophages; it is highly expressed in placenta and in serum of pregnant women; it may promote fetal survival by suppressing the production of maternally-derived proinflammatory cytokines within the uterus.--

10021650
123501
a112
Please replace the paragraph beginning at page 155, line 32, with the following:

--AAD2 Protein sequence (SEQ ID NO:114):
Gene name: Thrombospondin-1
Unigene number: Hs.87409
Probeset Accession #: AA232645
Protein Accession #: NP_003237.1
Signal sequence: predicted 1-18 (first underlined sequence)
Transmembrane Domain: none identified
Summary: Thrombospondin is a large modular glycoprotein component of the extracellular matrix and contains a variety of distinct domains, including three repeating subunits (types I, II, and III) that share homology to an assortment of other proteins.--

Please replace the paragraph beginning at page 155, line 66, with the following:

a113
--AAD9 protein sequence (SEQ ID NO:115):
Gene name: LIM homeobox protein cofactor (CLIM-1)
Unigene number: Hs.4980
Probeset Accession #: F13782
Protein Accession #: AAC83552
Pfam: LIM bind
Transmembrane Domain: none identified
Summary: The LIM homeodomain (LIM-HD) proteins, which contain two tandem LIM domains followed by a homeodomain, are critical transcriptional regulators of embryonic development. The LIM domain is a conserved cysteine-rich zinc-binding motif found in LIM-HD proteins, cytoskeletal components, LIM kinases, and other proteins. LIM domains are protein-protein interaction motifs, can inhibit binding of LIM-HD proteins to DNA, and can negatively regulate LIM-HD protein function.--

Please replace the paragraph beginning at page 156, line 21, with the following:

--AAE1 protein sequence (SEQ ID NO:116):

Gene name: guanine nucleotide binding protein 11

Unigene number: Hs.83381

Probeset Accession #: U31384

Protein Accession #: NP_004117.1

Pfam: G-gamma; CAAX motif (farnesylation site) prediction underlined

Summary: The G gamma proteins are a component of the trimeric G-proteins that interact with cell surface receptors. The G protein beta and gamma subunits directly regulate the activities of various enzymes and ion channels after receptor ligation. Unlike most of the other known gamma subunits, gamma 11 is modified by a farnesyl group and is not capable of interacting with beta 2.--

Please replace the paragraph beginning at page 156, line 37, with the following:

--AAE2 protein sequence (SEQ ID NO:117):

Gene name: Transcription factor 4 (Immunoglobulin transcription factor 2) (ITF-2) (SL3-3 Enhancer factor 2) (SEF-2)

Unigene number: Hs.289068

Probeset Accession #: M74719

Protein Accession #: NP_003190.1

Pfam: HLH domain prediction underlined

Summary: Transcription factor 4 is a helix-loop-helix (HLH) protein which belongs to a family of nuclear proteins, designated SL3-3 enhancer factors 2 (SEF2), that interact with an Ephrussi box-like motif within the glucocorticoid response element in the enhancer of the murine leukemia virus SL3-3. Various cell types display differences both in the sets of SEF2-DNA complexes formed and in their amounts. Molecular analysis of cDNA clones show the existence of multiple related mRNA species containing alternative coding regions, which are most probably a result of differential splicing.--

Please replace the paragraph beginning at page 156, line 68, with the following:

--AAE4 protein sequence (SEQ ID NO:118):

Gene name: phosphatidylcholine 2-acylhydrolase

Unigene number: Hs.211587

Probeset Accession #: M68874

Protein Accession #: AAA60105.1

Pfam: PLA2 B, C2 domain prediction underlined

Summary: Phospholipases A2 (PLA2s) play a key role in inflammatory processes through production of precursors of eicosanoids and platelet-activating factor. PLA2 is a 100 kd protein that contains a structural element homologous to the C2 region of protein kinase C.--

Please replace the paragraph beginning at page 157, line 26, with the following:

--ACA1 protein sequence (SEQ ID NO:119):

Gene name: tissue factor pathway inhibitor 2 TFPI2, placental protein 5 (PP5)
Unigene number: Hs.78045
Probeset Accession #: D29992
Protein Accession #: BAA06272.1
Pfam: Kunitz BPTI
Signal sequence: underlined
Summary: ACA1 is a serine proteinase inhibitor that was originally purified from conditioned medium of the human glioblastoma cell line T98G. ACA1 is identical to placental protein 5 (PP5) and TFPI2, a placenta-derived glycoprotein with serine proteinase inhibitor activity. PP5 belongs to the Kunitz-type serine proteinase inhibitor family, having three putative Kunitz-type inhibitor domains.--

Please replace the paragraph beginning at page 157, line 45, with the following:

--ACB8 protein sequence (SEQ ID NO:120):

Gene name: myosin X
Unigene number: Hs.61638
Probeset Accession #: N77151
Protein Accession #: NP_036466
Pfam: myosin head, IQ (calmodulin binding motif), PH, MyTH4
Summary: Myosins are molecular motors that move along filamentous actin. Seven classes of myosin are expressed in vertebrates: conventional myosin, or myosin-II, as well as the 6 unconventional myosin classes-I, -V, -VI, -VII, -IX, and -X.--

Please replace the paragraph beginning at page 158, line 24, with the following:

--ACC3 protein sequence (SEQ ID NO:121):

Gene name: calcitonin receptor-like (CALCRL)
Unigene number: Hs.152175
Probeset Accession #: L76380
Protein Accession #: NP_005786.1
Pfam: 7TM 2 (7 transmembrane receptor (Secretin family))
Transmembrane domains: predictions underlined
Signal sequence: first underlined region
Summary: Calcitonin gene-related peptide (CGRP) is a neuropeptide with diverse biological effects including potent vasodilator activity. The human CGRP1 receptor shares significant peptide sequence homology with the human calcitonin receptor, a member of the G-protein-coupled receptor superfamily. Stable expression in 293 (HEK 293) cells produces specific, high affinity binding sites for CGRP. Exposure of these cells to CGRP results in a 60-fold increase in cAMP production.--

Please replace the paragraph beginning at page 158, line 49, with the following:

--ACC5 protein sequence (SEQ ID NO:122):

Gene name: Selectin E (endothelial adhesion molecule 1)

Unigene number: Hs.89546

Probeset Accession #: M24736

Protein Accession #: NP_000441.1

Pfam: lectin c, EGF like domain, sushi (SCR domain)

Signal sequence: first underlined region

Transmembrane domain: second underlined region

Summary: Focal adhesion of leukocytes to the blood vessel lining is a key step in inflammation and certain vascular disease processes. Endothelial leukocyte adhesion molecule-1 (ELAM-1), a cell surface glycoprotein expressed by cytokine-activated endothelium, mediates the adhesion of blood neutrophils. The primary sequence of ELAM-1 predicts an amino-terminal lectin-like domain, an EGF domain, and six tandem repetitive motifs (about 60 amino acids each) related to those found in complement regulatory proteins. A similar domain structure is also found in the MEL-14 lymphocyte cell surface homing receptor, and in granule-membrane protein 140, a membrane glycoprotein of platelet and endothelial secretory granules that can be rapidly mobilized (less than 5 minutes) to the cell surface by thrombin and other stimuli. Thus, ELAM-1 may be a member of a nascent gene family of cell surface molecules involved in the regulation of inflammatory and immunological events at the interface of vessel wall and blood.--

Please replace the paragraph beginning at page 159, line 17, with the following:

--ACC8 protein sequence (SEQ ID NO:123):

Gene name: Chemokine (C-X-C motif), receptor 4 (fusin)

Unigene number: Hs.89414

Probeset Accession #: L06797

Protein Accession #: NP_003458.1

Pfam: 7TM 1 (7 transmembrane receptor (rhodopsin family))

Signal sequence: none identified

Transmembrane domains: predictions underlined

Summary: The chemokine receptor CXCR4 (also designated fusin and LESTR) is a cofactor for fusion and entry of T cell-tropic strains of HIV-1.--

Please replace the paragraph beginning at page 159, line 36, with the following:

--ACF2 protein sequence (SEQ ID NO:124):

Gene name: Endothelial cell-specific molecule 1

Unigene number: Hs.41716

Probeset Accession #: X89426

Protein Accession #: NP_008967.1

Signal sequence: underlined

Pfam: IGFBP (Insulin-like growth factor binding proteins)

Summary: Human endothelial cell-specific molecule (called ESM-1) was cloned from a human umbilical vein endothelial cell (HUVEC) cDNA library. Constitutive ESM-1 gene expression is seen in HUVECs but not in the other human cell lines. The cDNA sequence contains an open reading frame of 552 nucleotides and a 1398-nucleotide 3'-untranslated region including several domains involved in mRNA instability and five putative polyadenylation consensus sequences. The deduced 184-amino acid sequence defines a cysteine-rich protein with a functional NH2-terminal hydrophobic signal sequence.--

Please replace the paragraph beginning at page 159, line 58, with the following:

--ACF4 protein sequence (SEQ ID NO:125):

Gene name: P53-responsive gene 2 similar to D.melanogaster peroxidase(U11052)

Unigene number: Hs.118893

Probeset Accession #: D86983

Protein Accession #: BAA13219

Pfam: LRRNT (Leucine rich repeat N-terminal domain), LRR (Leucine Rich Repeat), LRRCT (Leucine rich repeat C-terminal domain), Ig (immunoglobulin domain), Peroxidase, VWC (von Willebrand factor type C domain)

Summary: ACF4 is a gene originally identified from KG-1 cell and brain cDNA libraries.--

Please replace the paragraph beginning at page 160, line 28, with the following:

--ACF5 protein sequence (SEQ ID NO:126):

Gene name: Mitogen-activated protein kinase kinase kinase 4

Unigene number: Hs.3628

Probeset Accession #: N54067

Protein Accession #: NP_004825.1

Pfam: pkinase (Eukaryotic protein kinase domain), CNH domain

Summary: The yeast serine/threonine kinase STE20 activates a signaling cascade that includes STE11 (mitogen-activated protein kinase kinase kinase), STE7 (mitogen-activated protein kinase kinase), and FUS3/KSS1 (mitogen-activated protein kinase) in response to signals from both Cdc42 and the heterotrimeric G proteins associated with transmembrane pheromone receptors. ACF5 is a human cDNA encoding a protein kinase homologous to STE20. This protein kinase, also designated HPK/GCK-like kinase (HGK), has nucleotide sequences that encode an open reading frame of 1165 amino acids with 11 kinase subdomains. HGK is a serine/threonine protein kinase that specifically activated the c-Jun N-terminal kinase (JNK) signaling pathway when transfected into 293T cells, but does not stimulate either the extracellular signal-regulated kinase or p38 kinase pathway. HGK also increased AP-1-mediated transcriptional activity in vivo. HGK may be a novel activator of the JNK pathway. The cascade may look like this: HGK -> TAK1 -> MKK4, MKK7 -> JNK kinase cascade, which may mediate the TNF-alpha signaling pathway.--

Please replace the paragraph beginning at page 161, line 4, with the following:

--ACF8 protein sequence (SEQ ID NO:127):

Gene name: Phospholipase A2, group IVC (cytosolic, calcium-independent)

Unigene number: Hs.18858

Probeset Accession #: AA054087

Protein Accession #: NP_003697.1

Pfam: none identified

Summary: ACF8 is a membrane-bound, calcium-independent PLA2, named cPLA2-gamma. The sequence encodes a 541-amino acid protein containing a domain with significant homology to the catalytic domain of the 85-kDa cPLA2 (cPLA2-alpha). cPLA2-gamma does not contain the regulatory calcium-dependent lipid binding (CaLB) domain found in cPLA2-alpha. cPLA2-gamma does contain two consensus motifs for lipid modification, a prenylation motif (-CCLA) at the C terminus and a myristoylation site at the N terminus. cPLA2-gamma demonstrates a preference for arachidonic acid at the sn-2 position of phosphatidylcholine as compared with palmitic acid. cPLA2-gamma encodes a 3-kilobase message, which is highly expressed in heart and skeletal muscle, suggesting a specific role in these tissues.--

Please replace the paragraph beginning at page 161, line 34, with the following:

--ACG1 protein sequence (SEQ ID NO:128):

Gene name: Carbohydrate (chondroitin 6/keratan) sulfotransferase 1

Unigene number: Hs.104576

Probeset Accession #: AA868063

Protein Accession #: NP_003645.1

Pfam: none identified

Summary: Chondroitin 6-sulfotransferase (C6ST) is the key enzyme in the biosynthesis of chondroitin 6-sulfate, a glycosaminoglycan implicated in chondrogenesis, neoplasia, atherosclerosis, and other processes. C6ST catalyzes the transfer of sulfate from 3'-phosphoadenosine 5'-phosphosulfate to carbon 6 of the N-acetylgalactosamine residues of chondroitin.--

Please replace the paragraph beginning at page 161, line 55, with the following:

--ACG5 protein sequence (SEQ ID NO:129):

Gene name: Multimerin

Unigene number: Hs.268107

Probeset Accession #: U27109

Protein Accession #: AAC52065

Signal sequence: prediction underlined

Pfam: EGF-like domain, C1q domain

Summary: Multimerin is a massive, soluble protein found in platelets and in the endothelium of blood vessels. Multimerin is composed of varying sized, disulfide-linked multimers, the smallest of which is a homotrimer. Multimerin is a factor V/Va-binding protein and may function as a carrier protein for platelet factor V. Northern analyses show a 4.7-kilobase transcript in cultured endothelial cells, a megakaryocytic cell line, platelets, and highly vascular tissues. The multimerin cDNA can encode a protein of 1228 amino acids with the probable signal peptide cleavage site between amino acids 19 and 20. The protein is predicted to be hydrophilic and to contain 23 N-glycosylation sites. The adhesive motif RGDS (Arg-Gly-Asp-Ser) and an epidermal growth factor-like domain were identified. Multimerin contains a probable coiled-coil structures in the central portion of its sequence. Additionally, the carboxyl-terminal region of multimerin resembles the globular, non-collagen-like, carboxyl-terminal domains of several other trimeric proteins, including complement C1q and collagens type VIII and X.--

Please replace the paragraph beginning at page 162, line 32, with the following:

--ACC6 protein sequence (SEQ ID NO:131):

Gene name: Homo sapiens cDNA FLJ11502 fis, clone HEMBA1002102, weakly similar to ANKRYIN

Unigene number: Hs.213194

Probeset Accession #: AA187101

Protein Accession #: none

Pfam: ankyrin repeats--

Please replace the paragraph beginning at page 162, line 45, with the following:

Q129
--ACC7 protein sequence (SEQ ID NO:132):
Gene name: Human RAL A gene
Unigene number: Hs.6906
Probeset Accession #: AA083572 cluster
Protein Accession #: P11233
Pfam: ras
Features: CAAX motif is underlined
Summary: The RALA gene encodes a low molecular mass ras-like GTP-binding protein that shares about 50% similarity with the ras proteins. GTP-binding proteins mediate the transmembrane signaling initiated by the occupancy of certain cell surface receptors. The RALA gene maps to 7p22-p15.--

10021656042001
Please replace the paragraph beginning at page 162, line 63, with the following:

Q130
--ACC9 protein sequence (SEQ ID NO:133):
Gene name: KIAA0955 protein
Unigene number: Hs.10031
Probeset Accession #: AA027168
Protein Accession #: BAA76799.1
Pfam: CARD (Caspase recruitment domain)
Summary: Gene was originally isolated as a brain cDNA. The coding region contains a CARD domain, suggesting involvement in apoptotic signaling pathways.--

10090412001
Please replace the paragraph beginning at page 163, line 14, with the following:

Q131
--ACF6 Protein sequence (SEQ ID NO:134):
Gene name: Homo sapiens cDNA FLJ10669 fis, clone NT2RP2006275, weakly similar to Microtubule-associated protein 1B [CONTAINS: LIGHT CHAIN LC1]
Unigene number: Hs.66048
Probeset Accession #: AA609717
Protein Accession #: BAA91743.1
Pfam: none identified
Summary: The cDNA for FLJ10669 was originally isolated from NT2 neuronal precursor cells (teratocarcinoma cell line) after 2-weeks of retinoic acid (RA) treatment. The protein sequence has similarity to microtubule-associated protein 1B (MAP-1B), suggesting a function for ACF6 in the regulating the cytoskeleton.--

Please insert the accompanying paper copy of the Sequence Listing, page numbers 1 to 154, at the end of the application.